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Distribution patterns of bottom trawl faunal assemblages in Porcupine bank: implications for Porcupine surveys stratification design

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1. Abstract

The distribution patterns of bottom trawl faunal assemblages in Porcupine bank is addressed using data from two bottom trawl surveys performed in the area. Hierarchical cluster analyses and canonical ordination analyses are applied respectively to define the different assemblages and to evaluate the main structuring environmental factors using information on depth, latitude, longitude, bottom temperature and salinity. Analyses are performed with two different matrices one in numbers of individuals per species in each haul and another in biomass of main commercial species in each haul. Three large assemblages are discriminated by hierarchical cluster analyses: shelf, outer-shelf and shelf-break, with some subgroups within each of them consistent in the results of both data matrices. Depth is the main structuring environmental factor in the area. Longitude has also an important effect on the bottom trawl assemblages distribution pattern, this effect is more likely to be related with relief structure and ground types differences in both sides of Porcupine bank. The original strata design used in Porcupine surveys, based on previous information on commercial catches, does not agree with the results of this study, but more information on the bathymetry in the area is needed to implement new bathymetric strata.

2. Introduction

Bottom trawl surveys are nowadays one of the most important methods to study commercial fishing stocks, given that they provide information independent from the fishery. These data play an important role to calibrate single species assessment models, used as a tool for fisheries management.

In 2001 Spain proposed a new survey to help overcome the current lack of sampling in some areas of the IBTS (International Bottom Trawl Survey) Western Division, and the IBTSWG acknowledged the advisability of carrying out such a survey. Since then two surveys have been performed in the Porcupine bank covering an area, previously without standardised surveys, from longitude 12º W to 15º W and from latitude 51º N to 54º N. Results of the first Porcupine survey were presented in Velasco and Sánchez (2002).

The sampling design used in this survey is random stratified and the strata were initially defined from data on catches of commercial hauls carried out in Porcupine area, collected within an IEO Discard Sampling project. The data from the two surveys already performed allow studying the species distribution and the main factors driving the structure and distribution of the bottom trawl faunal assemblages in the area. With the results of the performed analyses the suitability of initial stratification is addressed, in an attempt to improve the initial sampling design, according to the assumptions of the random stratified sampling design, by reducing the intra-stratum variance and maximising inter-strata variance.

3. Material and methods

The area covered in Porcupine surveys is the Porcupine bank extending from longitude 12° W to 15° W and from latitude 51° N to 54° N, covering depths between 180 and 800 m. The cruises were carried out in September 2001 and 2002 on board R/V “Vizconde de Eza”, a stern trawler of 53 m and 1800 Kw.

The sampling gear used is the Porcupine baca 40/52, a high headline modification of the Baca Trawl routinely used in bottom trawl surveys off the Atlantic Spanish Coast described in ICES (2003). During the surveys, mean vertical opening of the net was around 3.5 m, horizontal opening 17-21 m, and door spread 120 m. Towing speed was set to 3.5 kn and hauls lasted 30 min between the end of wire shutting and starting to pull it back.

Information on catches of commercial hauls carried out in Porcupine area, collected in a Discard Sampling project, was used to design sampling strategy. Finally it was decided to use a random stratified sampling as shown in Figure 1, with two area strata or sectors and three depth strata defined by the 200, 400 and 800 m isobaths, resulting in 5 strata, given that there are no grounds shallower than 200 m in Sector 2. Total area was divided in 5×5 nm squares and a total number of 78 and 86 valid hauls were carried out in 2001 and 2002 surveys respectively, making up a sampling coverage of around 1 sampled square of each 6 squares. At the beginning of the first survey three special hauls were performed to test the gear performance and decide trawling duration, these hauls are used in the general description of distribution patterns but not to estimate stratified biomass indices. Final haul distribution per survey and strata are summarised in Table 1.

In every haul catch was sorted to species level. Total catch of every species was weighed and length distribution of every fish species was obtained to the inferior centimetre, nephrops was measured to the inferior millimetre. Other invertebrates were only weighed and counted. Otoliths of hake and megrim were collected to obtain age-length keys to estimate abundance indices per age group for these species, 2001 survey ALKs were used for both years because 2002 ALKs were not available.

Besides a hydrographical sampling was carried out with a Seabird-25 CTD, performing a CTD cast at the end of every haul. Some additional samples were collected to cover the gaps due to the random stratified sampling used in the fishes, and also to cover the central non trawlable area.

Data processing was done on board using CAMP 10.2 software.

Abundance index used was mean stratified catch per 30 minutes haul, these indices are independent for every stratum and are equivalent to the expected yield in each stratum. (1) Mean stratified catch, and (2) Stratified Variance:

$$(1) \qquad \overline{Y}_{st} = \frac{1}{A}\sum A_h \overline{Y}_h \qquad\qquad (2) \qquad S^2_{(\overline{Y}_{st})} = \frac{1}{A^2}\sum \frac{A_h^2 S_h^2}{n_h},$$

being A total area; A_h stratum h area; Y_h mean catch by haul in stratum h, n_h number of hauls in stratum h and S_h^2 variance in stratum h. (Cochran, 1971; Grosslein and Laurec, 1982).

Hierarchical cluster analysis was used to define the main megafaunal communities in the area and their distribution. With this purpose a matrix with number of individuals per species and haul was built, including all the species captured in more than a 5% of the hauls but some invertebrates of which the determination was not consistent in both surveys. Given that estimating abundance indices of commercial species are one of the main objectives of Porcupine survey, a second matrix in biomass terms was built including only commercial species and the most abundant fish species (including some deep species to ensure the discrimination of deep stations). In both matrices hake and megrim were included in number/biomass per age group (0 to 9+).

These matrices were log-transformed to decrease the weight of the most abundant species and samples, and similarity matrices were calculated using Bray & Curtis similarity index, dendrograms were subsequently obtained with group average aggregation algorithm. SIMPER analysis was used to examine the contribution of each species to the average Bray-Curtis dissimilarity between groups of samples and the contribution to similarity within a group. All these analysis were performed with the Primer 5 software package (Clarke & Warwick 1994; Field & al. 1982).

To investigate the relation between faunal distribution patterns and environmental variables, canonical ordination analyses were applied to the same matrices using depth, latitude, longitude and bottom temperature and salinity as environmental factors (using the program CANOCO.4.5). Canonical test used was Redundancy Analysis, RDA (Ter Braak & Wiertz, 1994). With canonical techniques, ordination axes are constrained to be linear combinations of the environmental variables used in the analysis. The diagram obtained is a simultaneous ordination of species, sites and environmental

variables. Ordination significance is given in terms of axis *eigenvalues* and variance explained. Within the RDA procedure, Montecarlo permutation tests were used to test the significance of the analysis (Verdonschot & Ter Braak, 1994). The underlying theory of these methods is presented in Jongman *et al.* (1987) and Ter Braak & Smilauer (1998).

4. Results

A comprehensive list of species and their total abundance indices in biomass and numbers during 2001 and 2002 surveys are provided in Annex 1, together with maps showing the spatial distribution of main commercial species (and some abundant species as *Argentina silus* or *Mora moro*) within the Porcupine bank area.

4.1. Distribution and structure of megafaunal communities

At a similarity level of 45% the dendrogram in terms of number shows three clusters of samples (Figure 2). The structure reveals a bathymetric stratification with boundaries at 450 and 530 m depth, delimiting a Shelf cluster (samples at depths shallower than 450 m), an Outer Shelf cluster (450-530 m) and Shelf-Break cluster (> 530 m).

The first dichotomy separates the Shelf-Break group from Shelf and Outer Shelf groups. The shallowest group is typified by *M. poutassou, G. argenteus, A. silus* and *H. dactylopterus* (35 % similarity intragroup), while Shelf-Break cluster is typified by *L. eques, M. poutassou, A. silus* and *P. blennoides* (35 % similarity intragroup). An 18 % of the dissimilarity between both groups is due to *G. argenteus, M. poutassou* and *L. boscii* (with higher densities in shelf and outer shelf group) and *L. eques*, the crab *G. longipes* and the sea urchin *P. placenta* (with higher densities in shelf-break group).

The second dichotomy segregates Shelf samples from Outer Shelf Samples. The Shelf group is typified by *M. poutassou, G. argenteus, A. silus* and *H. dactylopterus* (33 % similarity intragroup), while the Outer Shelf group is typified by *M. poutassou, D. bonnieri, P. blennoides* and *N. norvegicus* (40 % similarity intragroup). Dissimilarity between both groups is due in a 17 % to *L. boscii, L. whiffiagonis* 2-4 and *G. argenteus* (with higher densities in shelf group) and *N. norvegicus* (with higher densities in outer shelf group).

Below this similarity level, 8 groups can be defined (Figure 2), groups 1-5 belong to the Shelf cluster, the Outer Shelf cluster makes up group 6, and groups 7-8 belong to Break-shelf cluster. Figure 3 shows the location of dendrogram groups in the area, while Table 2 shows the species that typified groups, through similarity intragroups and dissimilarity intergroups.

- Group 1: clusters samples of depths between 200-300 m. Typified by *M. aeglefinus, T. esmarckii* and *G. argenteus* (Table 2). Located in the eastern part of Porcupine bank next to the Irish shelf (Figure 3).
- Group 2: it also contains samples of depths between 200-300 m, but is typified by *A. richardi, M. variegatus* and *L. whiffiagonis* 1-4 age groups. Geographically differs from the previous group because it is located around the central rocky head of Porcupine bank, westernwards of group 1 (Figure 3).
- Group 3: samples from depths between 300 and 400 m. Typified by *M sarsi* and *L. boscii*, and located in the northern part surrounding the rocky head and Group 2 samples.
- Group 4: deeper samples of Shelf cluster (300-450 m), typified by *C. coelorhynchus*, the shrimp *D. bonnieri* and the sea urchin *S. purpureus*. It is located in the southern part of the Shelf cluster zone
- Group 5: formed by two outsider samples related with the two preceding groups. Typified by *E. spinax*, sea star *L. sarsi* and spider crab *M. tenuirrostris* and located in the area known by Spanish fishermen as the 53º Turnabout.
- Group 6: sole group of Outer Shelf cluster (450-530 m). Typified by *D. bonnieri, N. norvegicus* and the shrimp *P. sivado*. Located in the southern part of the area between Shelf and Shelf-Break areas, from 53º Turnabout southward covering a smoothly descending slope with mud grounds especially suitable for nephrops.

Within the Break-Shelf cluster (>530 m) there are two groups with a longitude frontier around 14ºW in the southernmost part of the bank:

- Group 7: western group characterised by a steeper slope from 400 m onward. Typified by *L. eques, G. longipes* and *P. multidentata*.
- Group 8: eastern group located following Group 6 and also characterised by mud grounds. Typified by also by *L. eques,* and species from muddy grounds as sea urchin *P. placenta* and sea cucumber *S. tremulus.*

4.2. Environmental affinities of megafaunal communities

The canonical analysis performed with the number data matrix shows depth as main structuring factor, with a high correlation with Axis 1 (Table 4). Axis 2 is mainly correlated with Longitude that is the second structuring factor, but explaining lower variance as is revealed by the difference between the *eigenvalues* of both axes. Figure 4 (a) shows the arrangement of samples (represented with the same symbols than cluster groups in other figures) in relation to environmental gradients, wherein is clear the depth influence. Regarding longitude there is an east-west discrimination for all groups, but for Group 3 made evident by its dispersion throughout the whole Axis 2 range.

The arrangement of species (Figure 4 b) confirms the affinities shown in Table 2. Axis 1 produces a depth-related distribution of species. The more discriminated species with depth are all *L. whiffiagonis* age groups, *G. argenteus, M. poutassou, L. boscii* and *G. cynoglossus*, in shallowest depths, and *L. eques, G. longipes, S. kaupi, T. scabrus, E. telescopus* and *M. moro* in deepest areas. Species with a wide bathymetric range are located near the centroid (age group 5 of *M. merluccius, D. bonnieri*) or species inhabiting in the middle range of the gradient. Concerning Axis 2, *T. esmarckii, M. aeglefinus* and age groups 2 and 3 of *M. merluccius* show affinity with eastern-longitudes (related with Group 1). On the other hand, several species are correlated with western-longitudes, especially *C. coelorhynchus, P. placenta, M. moro, H. dactylopterus* and *A. silus*.

4.3. Distribution and structure of main commercial species

Regarding commercial species, a similar structure arises from the cluster analyses. The most remarkable difference is the affinity of Outer Shelf cluster, which in this case is grouped with the Shelf-break cluster instead of Shelf cluster, as in the total megafauna numbers data. As in the former analysis, 8 groups can be defined (Figure 5) and its spatial distribution is shown in Figure 3 (b).

- Group 1: analogous to Group 2 of total megafauna analysis. Typified by thickback sole (*M. variegatus*) and lemon sole (*M. kitt*).
- Group 2: analogous to Group 1 of total megafauna analysis and also in this case typified by the haddock (*M aeglefinus*) and norway pout (*T. esmarckii*).
- Group 3: analogous to Group 3 of total megafauna analysis. Typified by *T. trachurus* and *M. molva*. Located in the same area of total megafauna group 3, except in the westernmost area of the central rocky head, where the samples belong to group 1, instead of to group 3.
- Group 4: analogous to Group 4 of total megafauna analysis. Typified by *A. silus* and *H. dactylopterus*.
- Group 5: could be considered as an extension of group 5 in total megafauna analysis, including also part of group 6 samples. Typified by *E. spinax,* nephrops and *L. boscii*. Located in the 53º Turnabout.
- Group 6: Analogous to Group 6 of total megafauna analysis except for the samples of the preceding group. Typified by several ubiquitous species (*M. poutassou, A. silus, P. blennoides* and *H. dactylopterus*).

Regarding the Shelf-Break group, in this analysis the geographical discrimination is latitudinal (around the 53º N), whereas in the total analysis a longitudinal separation (around 14ºW) is found.

- Group 7: Shelf-break group southwards 53ºN. Typified by *L. eques*.
- Group 8: Shelf-break group northwards 53ºN. Typified by *L. eques,* and distinguished from the later cluster by the higher abundances of *D. calceus* and *M. moro*.

Group 9 in Figure 3 (b) is not considered as a group given that it is constituted solely by an outsider sample locate among the group 5 samples. This sample is characterised by very low catches in biomass terms.

4.4. Environmental affinities of commercial fish populations

The importance of environmental variables in axes construction is practically the same that in the case of the analysis in number terms, with depth as the main driving factor and longitude as the second one (Table 5).

Figure 6 (a) represents the arrangement of samples and it is also evident the depth influence on cluster correspondence. Longitude discrimination is clearer in shallower cluster groups but not evident in the deeper ones revealing the broad longitude range occupied by group 7.

The arrangement of commercial species (Figure 6 b) is identical to the one shown in Figure 4 (b). Curiously, some commercial species, especially blue whiting, very wide-spread in Porcupine area present a clear correlation towards shallower depths (in total number as in biomass commercial analyses), which may be explained by their much higher abundances in these shallower areas compared to deeper ones (e.g. see spatial distribution of *M. poutassou* annex 1).

5. Discussion

The results of this study show that depth is the most important environmental factor driving the megafaunal species distribution patterns in Porcupine bank area, this bathymetric defined structure common pattern has been already described in previous studies carried out in other areas (Lauroz, 1993; Sánchez, 1997; Fariña et al., 1997; Gaertner et al.,1998; Souissi et al, 2001). Besides this bathymetric structure there is also an important effect of longitude on distribution patterns, this effect is more likely related to the different slope relieves and ground types in both sides of Porcupine bank, with steep slopes in the western part and shelving slopes and muddy grounds in the south-eastern part. Other environmental factors as bottom temperature and salinity have little importance as structuring factors of the distribution patterns of the bottom trawl fauna assemblages in the area.

5.1. Suitability of the initial stratification:

According to the results of these analyses there is no evident support to the original division of geographical sectors (Figure 1). Examining the analyses performed with data on commercial species and the distribution shown in Figure 3 (b), a new stratification with two geographical strata defined by a frontier between northern and southern sectors at 52º40’ N would be more suitable to the distribution patterns found.

Regarding bathymetric strata it is also evident that the 200 m limit of the shallowest stratum does not correspond to an actual frontier for the distribution patterns found in the analyses, and taking into consideration the reduced size of this stratum it is advisable to remove this depth limit. Furthermore, two bathymetric limits are defined by the performed analyses, one around 300 m splitting the shelf from the outer shelf and another one around 450 m delimiting the shelf break. The problem faced to implement the resulting strata is the current lack of information on the bathymetry in the area, that does not allow calculating the strata limits and their total area, needed to estimate stratified abundance and biomass indices. Therefore further changes in bathymetric strata will be reconsidered if new information on bathymetry is available. Also the differences between the old stratified abundance indices and those arising from a new stratification will be assessed before taking a decision paying special attention to intra-stratum and inter-strata variability of the indices with different possible stratifications.

6. Acknowledgments

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7. References

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8. Tables

Table 1.- Number of hauls carried out in Porcupine surveys by strata and year

	2001 Survey			2002 Survey		
	Sector 1	Sector 2	Total	Sector 1	Sector 2	Total
100-200 m	2		2	2		2
201-400 m	18	22	40	21	22	43
401-800 m	21	15	36	24	17	41
Total	41	37	78	47	39	86

Table 2. SIMPER analysis. Most contributing species to intragroups similarity (first square of every column) and intergroups dissimilarity (rest of squares). Species in bold type are more abundant in horizontal cluster, the rest in the vertical cluster (the list of the codes used in this table is included in annex 1)

	Group 1	Group 2	Group 3	Group 4	Group 5	Group 6	Group 7	Group 8
Group 1	*Mpou* *Garg* *Asil* *Wf* 2,3,4							
Group 2	*Maeg* *Tesm* ***Aric*** *Pble*	*Mpou* *Asil* *Wf* 1,2,3,4 *Mvar*						
Group 3	*Maeg* ***Ccoe*** ***Msar*** ***Ttra***	*Mvar* *Ttra* ***Ccoe*** *Aric*	*Mpou* *Garg* *Asil* *Hdac*					
Group 4	***Ccoe*** *Maeg* *Tesm* *Wf* 1,2	*Mvar* ***Ccoe*** *Aric* *Wf* 1,2	***Msar*** *Asil* ***Aric*** *Spur*	*Mpou* *Asil* *Garg* *Hdac*				
Group 5	*Asil* *Wf* 1,2 *Tesm* *Maeg*	*Asil* *Mvar* *Wf* 1,2 *Ttra*	*Asil* *Msar* ***Espi*** *Mlae*	*Asil* *Ccoe* *Hdac* *Mlae*	*Mpou* *Garg* *Lsar* *Espi*			
Group 6	*Wf* 2,3,4 *Maeg* *Tesm* ***Nnor***	*Wf 1,2,3,4* *Mvar* *Aric* ***Dbon***	*Lbos* ***Nnor*** *Msar* *Wf* 2,3,4	*Lbos* *Asil* *Ccoe* *Lsar*	***Asil*** *Lsar* ***Nnor*** *Wf* 4	*Mpou* *Dbon* *Pble* *Nnor*		
Group 7	*Garg* ***Lequ*** ***Glon*** *Wf* 3	*Wf* 2,3,4 ***Lequ*** *Garg* *Mvar*	*Garg* ***Lequ*** ***Glon*** *Lbos*	*Garg* ***Lequ*** ***Glon*** *Lbos*	***Lequ*** ***Glon*** *Garg* ***Asil***	***Lequ*** *Nnor* **Glon** *Garg*	*Lequ* *Mpou* *Asil* *Glon*	
Group 8	*Garg* ***Lequ*** ***Ppla*** *Maeg*	*Aric* ***Lequ*** *Garg* *Wf* 2,3,4	*Garg* ***Lequ*** ***Ppla*** *Lbos*	*Garg* ***Lequ*** ***Ppla*** *Lbos*	***Lequ*** ***Ppla*** *Garg* ***Asil***	***Ppla*** ***Lequ*** *Dbon* *Nnor*	***Ppla*** ***Ccoe*** ***Stre*** ***Asil***	*Lequ* *Mpou* *Hdac* *Ppla*

Table 3. SIMPER analysis with data in biomass. Most contributing species to intragroups similarity (first square in every column) and intergroups dissimilarity (rest of squares). Species in bold type are more abundant in horizontal cluster, the rest in the vertical cluster (the list of the codes used in this table is included in annex 1)

	Group 1							
Group 1	Mpou Asil Lpis Gcyn	Group 2						
Group 2	**Maeg** **Tesm** **Hk 2 (3)** **Pble**	Mpou Asil Maeg Wf 4,3,6	Group 3					
Group 3	Ttra Mvar **Pble** Mkit	Maeg Ttra Mkit Lbud	Mpou Hdac Asil Pble	Group 4				
Group 4	**Pble** Mvar Mkit Ttra	Maeg Tesm Hk 2 **Gmel**	Mmol Ttra **Nnor** **Gmel**	Mpou Asil Hdac Pble	Group 5			
Group 5	Ttra Mvar Wf 1 Mkit	Tesm **Espi** Ttra Wf 1	Mmol **Nnor** **Espi** Wf 2	Hk 8 **Espi** Hk 7,9 Asil	Mpou Lpis Hdac Pble	Group 6		
Group 6	Wf 4,3,2,5,6 Mvar Wf 1 **Pble**	Maeg Wf 4, 3 Tesm Wf 2,6,5	Lbos Wf 4,3,2,5,6 Mmol Wf 7	Lbos Wf 4 Gcyn **Lequ**	**Hk 8** Lbos **Lequ** Wf 5,6	Mpou Asil Pble Hdac	Group 7	
Group 7	**Lequ** Ttra Wf 4,3,2,5,6 **Pble**	**Lequ** Maeg Wf 4 **Gmel**	**Lequ** Lbos Wf 4,3,5,6 Gcyn	**Lequ** Lbos Gcyn Wf 4	**Lequ** **Hk 8** Lbos **Gmel**	**Hmed** **Lequ** Nnor **Mmor**	Asil Pble Lequ Mpou	Group 8
Group 8	Asil **Lequ** **Dcal** Wf 3	**Lequ** Asil Maeg **Dcal**	**Lequ** **Dcal** Asil **Mmor**	Asil **Lequ** **Dcal** **Mmor**	**Lequ** **Dcal** **Mmor** Hk 5,4,6	Asil **Dcal** Hk 6,7 (5) **Mmor**	Asil Hk 7,6,8 **Dcal** **Gcyn**	Lequ Hdac Pble Mpou

Table 4. Inter set correlations of environmental variables with the two first axes in the analysis with data in number terms.

Environmental factor	Axis 1	Axis 2
Depth	0.9538	0.0463
Latitude	-0.6012	0.0834
Longitude	0.2950	-0.7320
Bottom Temperature	-0.1628	0.4724
Bottom Salinity	-0.0832	0.1146

Table 5. Inter set correlations of environmental variables with the two first axes in the analysis with data in biomass of commercial species

Environmental variable	Axis 1	Axis 2
Depth	0.9347	0.1170
Latitude	-0.6465	0.2170
Longitude	0.3412	-0.7268
Bottom Temperature	-0.1794	0.4489
Bottom Salinity	-0.0923	0.1525

9. Figures

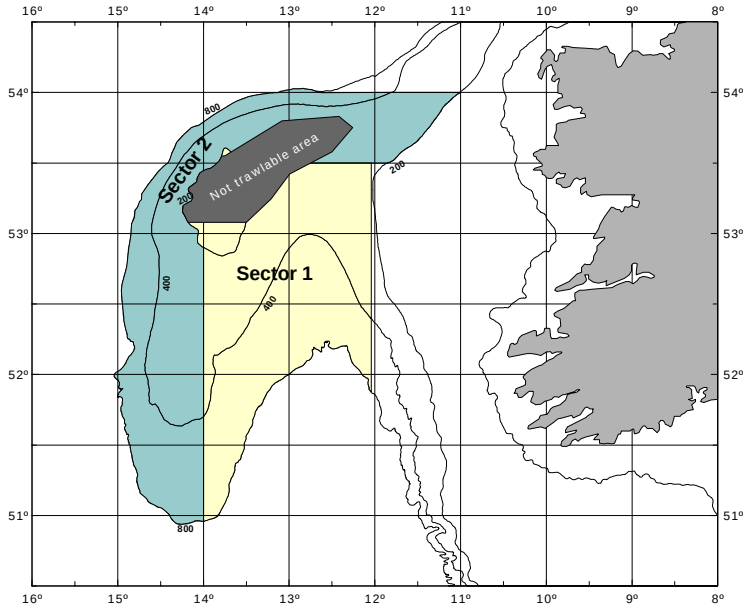

Figure 1.- Stratification used in Porcupine 0901 survey. Depth strata were a) shallower than 200 m, b) 200 – 400 m and c) 400 – 800 m. The grey area in the middle of Porcupine bank corresponds to a large non trawlable area not considered for area measurements and stratification

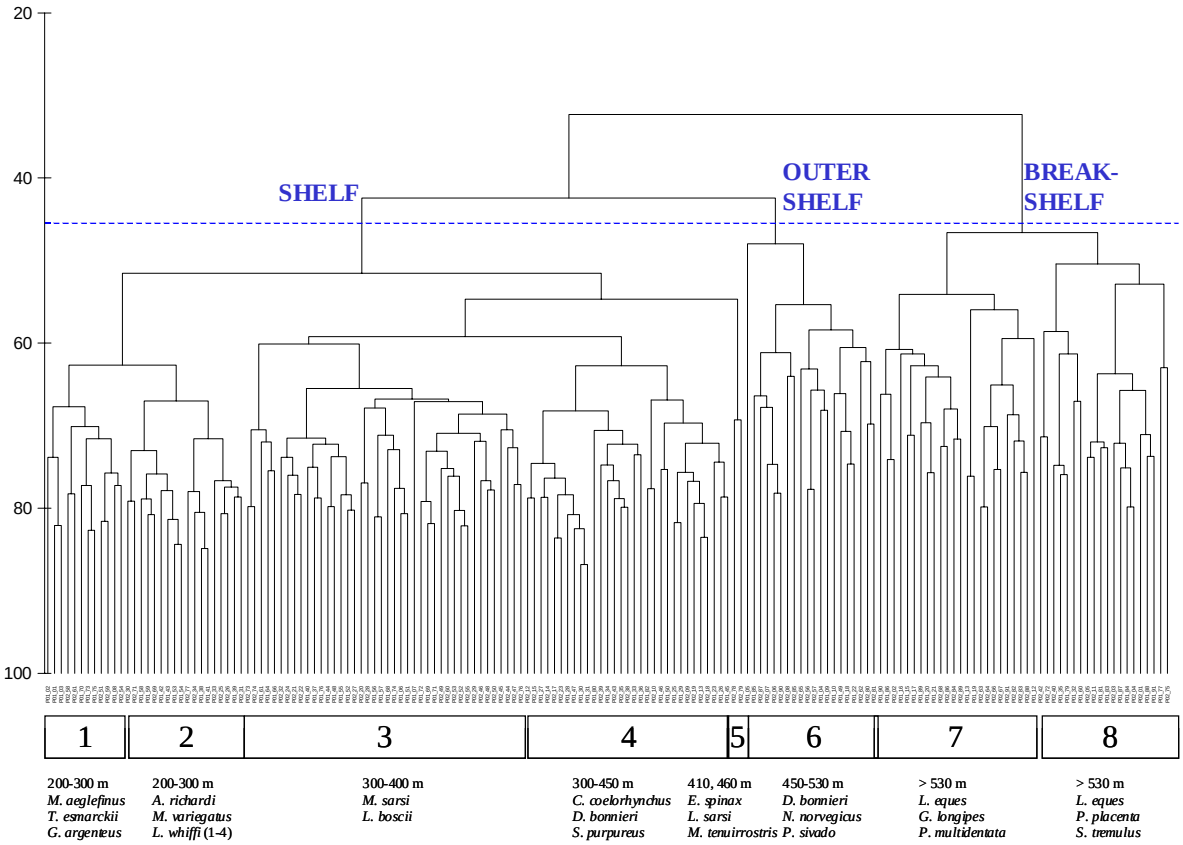

Figure 2. Dendrogram of samples with number of species (Bray-Curtis similarity index and Log transformed data) showing the main clusters, depth ranges and the typifying species

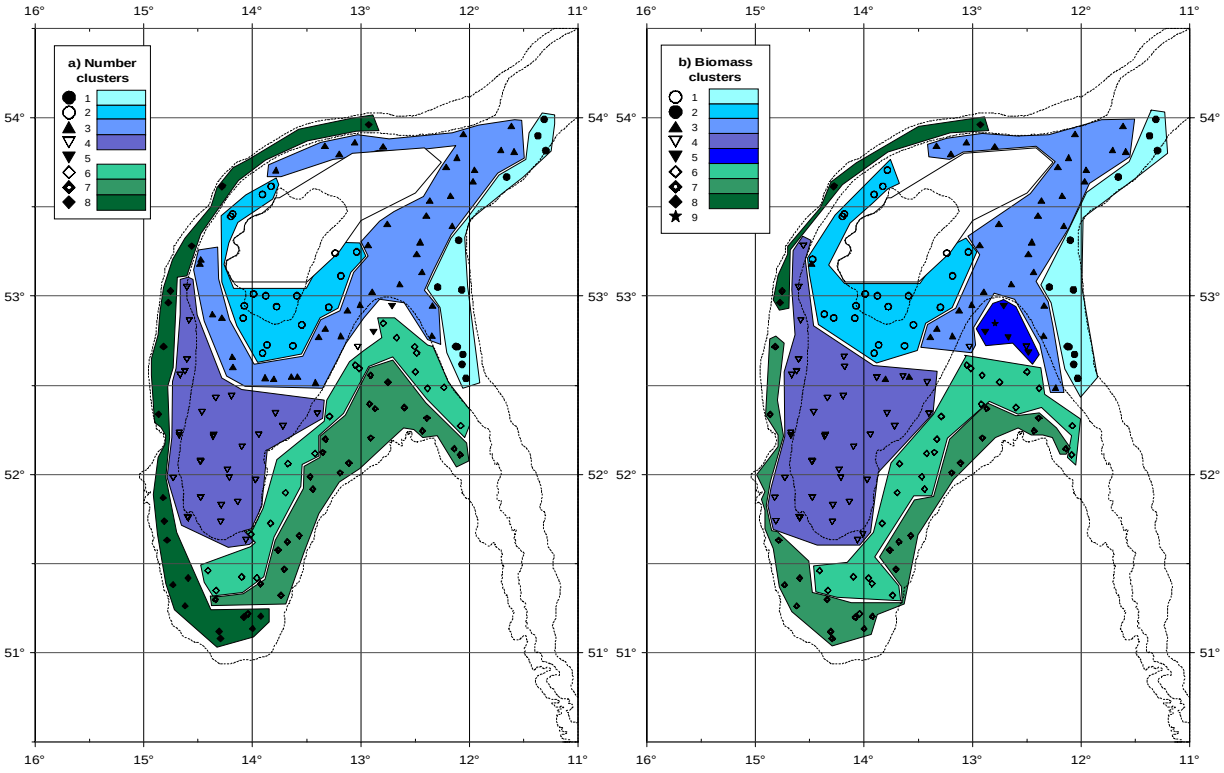

Figure 3. Spatial distribution of cluster groups: **a)** Clusters arising from analysis with data in terms of number and **b)** with data in biomass of commercial species

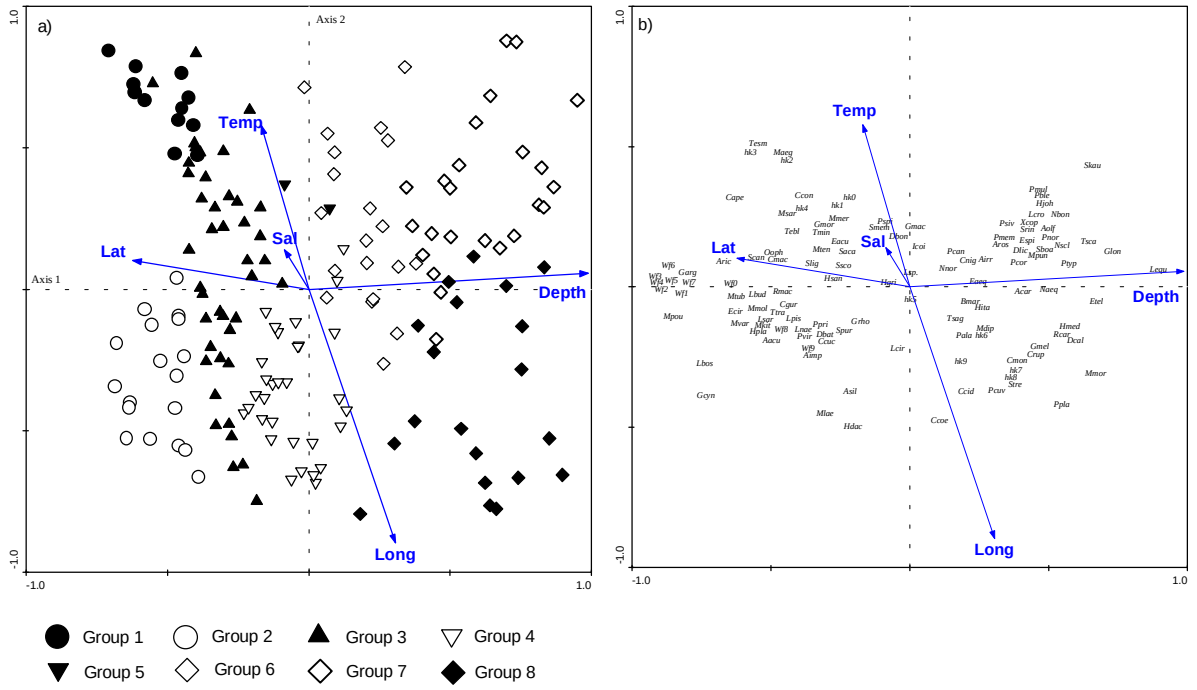

Figure 4. RDA analysis on total species number of individuals, log transformed. a**)** Biplot of environmental variables vs. sites. **b)** Biplot of environmental variables vs. species. Percentage of explained variance= 34.9 (species data), 88.2 (species-environment relation). Eigenvalues: 0.301 (Axis 1), 0.048 (Axis 2). Montecarlo test of significance of first axis- p=0.002. (Lat: Latitude, Long: West Longitude, Temp: Bottom temperature, Sal: Bottom salinity. The list of the species codes used in this figure is included in annex 1)

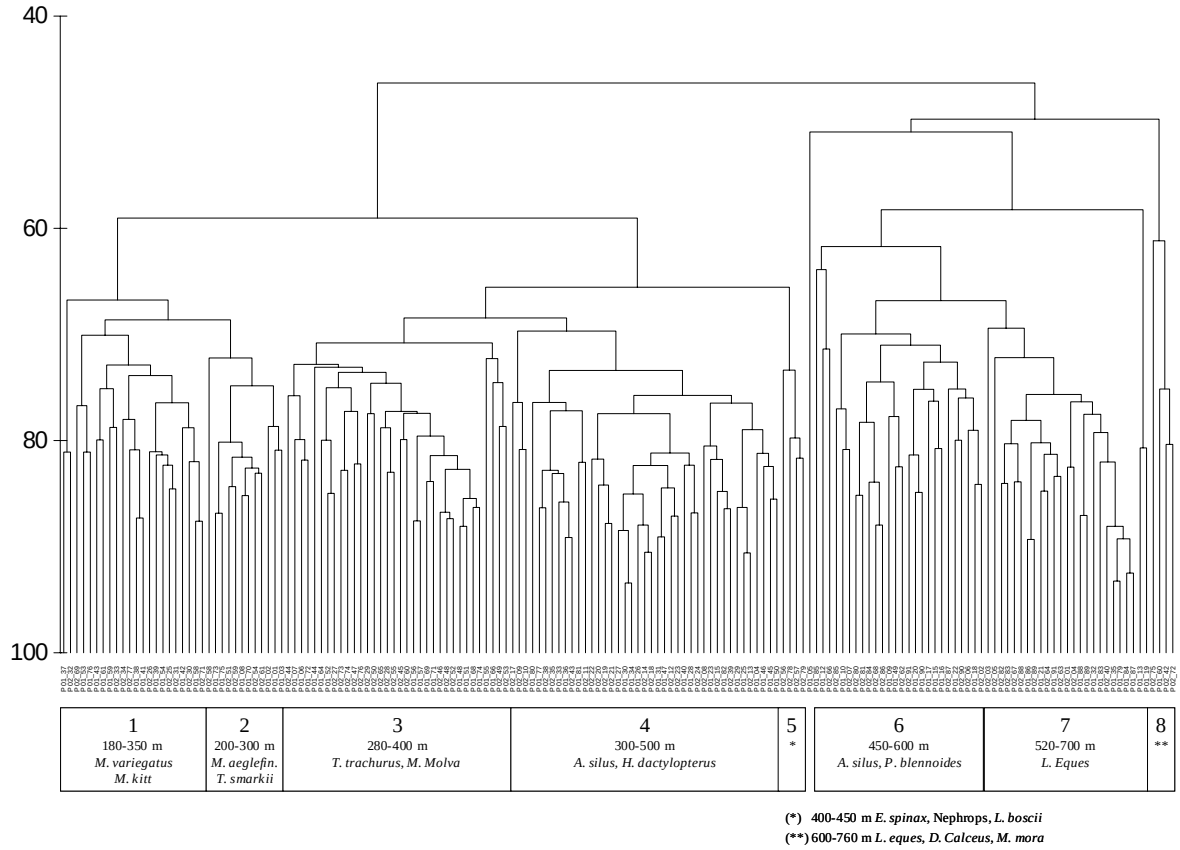

Figure 5. Dendrogram of samples from commercial species data (Bray-Curtis similarity index and Log transformed data) showing the main clusters, depth ranges and the typifying species

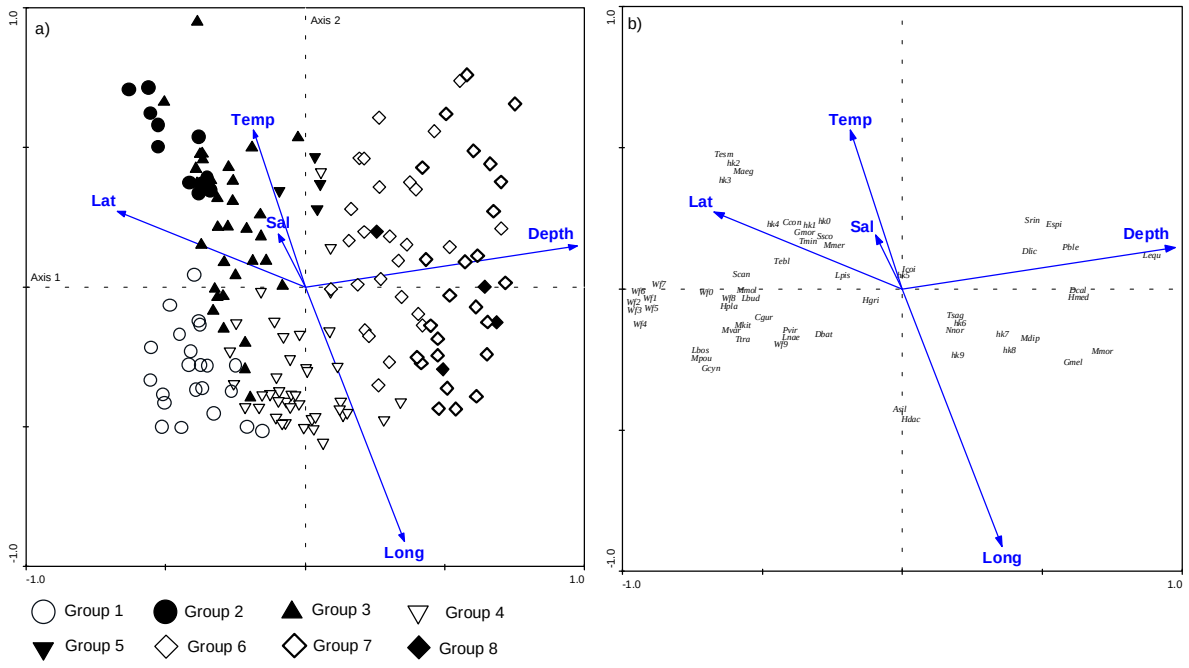

Figure 6. RDA analysis on commercial species biomass log transformed matrix. **a)** Biplot of environmental variables vs. sites (commercial species). **b)** Biplot of environmental variables vs. commercial species. Percentage of explained variance: 35.3 (species data), 92.3 (samples-environment relation). Eigenvalues: 0.322 (Axis 1), 0.031 (Axis 2). Montecarlo test of significance of first axis p=0.002. (Lat= N Latitude, Long= W Longitude, Temp= Bottom temperature, Sal= Bottom salinity. The list of the species codes used in this figure is included in annex 1)

10. Annex1. List of species and main commercial species spatial distribution

Table 6. List of species. C: species included in commercial species matrix (yes, no). Tot: species included in total species number matrix. Code: code used in figures and tables. Average and standard deviation of the catch in all the hauls performed in both surveys, in biomass and number terms. %Pres: percentage of total hauls in both surveys in which the species was captured.

				Biomass (gr)		Number		% Pres
C	**Tot**	**Code**	**Scientific name**	**Avg.**	**Std. Dev.**	**Avg.**	**Std. Dev.**	
Y	Y	Asil	*Argentina silus*	140207.8	374189.7	1024.95	2147.08	97.0
Y	Y	Cgur	*Chelidonichthys gurnardus*	1690.9	8216.9	5.65	28.87	13.0
Y	Y	Ccon	*Conger conger*	704.6	1601.9	0.52	1.07	30.2
Y	Y	Dlic	*Dalatias licha*	121.8	351.7	0.25	0.68	16.0
Y	Y	Dcal	*Deania calceus*	3545.1	24691.8	1.58	9.41	12.4
Y	Y	Dbat	*Dipturus batis*	701.3	3463.1	0.12	0.47	8.9
Y	Y	Espi	*Etmopterus spinax*	813.2	2219.6	5.74	14.09	37.9
Y	Y	Gmor	*Gadus morhua*	257.3	1697.3	0.07	0.33	4.7
Y	Y	Gmel	*Galeus melastomus*	6161.7	19565.2	16.78	37.35	71.0
Y	Y	Gcyn	*Glyptocephalus cynoglossus*	3554.9	8608.7	21.58	58.12	79.9
Y	Y	Hdac	*Helicolenus dactylopterus*	17558.5	39384.8	109.42	193.60	100.0
Y	Y	Hgri	*Hexanchus griseus*	767.6	3996.3	0.18	0.62	10.7
Y	Y	Hpla	*Hipoglossoides platessoides*	514.3	1824.2	6.26	26.49	29.6
Y	Y	Hmed	*Hoplostethus mediterraneus*	1136.8	6011.7	4.14	22.30	12.4
Y	Y	Icoi	*Illex coindetii*	25.7	103.6	0.18	0.65	9.5
Y	Y	Lequ	*Lepidion eques*	7374.0	20304.6	73.07	168.33	30.2
Y	Y	Lbos	*Lepidorhombus boscii*	5165.0	7362.9	64.85	104.74	71.0
Y	Y	Wf0	*Lepidorhombus whiffiagonis* age 0	55.7	166.3	4.99	14.50	36.1
Y	Y	Wf1	*L. whiffiagonis* age 1	359.8	856.8	17.84	43.23	59.2
Y	Y	Wf2	*L. whiffiagonis* age 2	871.2	1759.4	30.70	64.01	65.1
Y	Y	Wf3	*L. whiffiagonis* age 3	1246.8	2281.5	35.65	66.33	67.5
Y	Y	Wf4	*L. whiffiagonis* age 4	1871.9	3554.4	34.54	63.45	69.2
Y	Y	Wf5	*L. whiffiagonis* age 5	1074.0	2188.7	13.78	27.79	69.2
Y	Y	Wf6	*L. whiffiagonis* age 6	1030.9	1939.6	10.43	20.88	68.0
Y	Y	Wf7	*L. whiffiagonis* age 7	468.0	851.6	2.24	3.82	62.1
Y	Y	Wf8	*L. whiffiagonis* age 8	277.6	650.4	0.58	1.30	35.5
Y	Y	Wf9	*L. whiffiagonis* age 9+	137.2	490.7	0.18	0.59	22.5
N	N	-	*L. whiffiagonis* Total	7002.1	11939.5	150.81	286.19	69.8
Y	Y	Lnae	*Leucoraja naevus*	265.5	1005.4	0.41	1.66	9.5
Y	Y	Lbud	*Lophius budegassa*	561.5	1441.3	0.45	1.01	21.9
Y	Y	Lpis	*Lophius piscatorius*	6455.9	7818.9	3.83	5.02	81.1
Y	Y	Maeg	*Melanogrammus aeglefinus*	3064.2	13003.4	33.56	182.65	31.4
Y	Y	Mmer	*Merlangius merlangus*	50.7	378.9	0.09	0.64	3.0
Y	Y	hk0	*Merluccius merluccius age 0*	2.9	14.9	0.42	2.39	6.5
Y	Y	hk1	*M. merluccius* age 1	17.0	90.9	0.20	1.08	6.5
Y	Y	hk2	*M. merluccius* age 2	154.9	572.6	0.59	2.32	27.2
Y	Y	hk3	*M. merluccius* age 3	658.3	1432.1	1.62	3.74	55.6
Y	Y	hk4	*M. merluccius* age 4	903.7	1280.2	1.46	2.10	77.5
Y	Y	hk5	*M. merluccius* age 5	1707.0	2296.8	1.87	2.53	85.2
Y	Y	hk6	*M. merluccius* age 6	2948.2	5877.0	2.31	4.07	85.2
Y	Y	hk7	*M. merluccius* age 7	2889.9	9092.2	1.56	4.84	72.8
Y	Y	hk8	*M. merluccius* age 8	1629.2	5122.3	0.85	2.65	68.6
Y	Y	hk9	*M. merluccius* age 9+	1168.4	4151.8	0.39	1.36	46.7
N	N	-	*M. merluccius* Total	10977.9	20847.4	11.29	15.46	94.1
Y	Y	Mvar	*Microchirus variegatus*	790.5	3091.2	23.19	87.75	24.3
Y	Y	Mpou	*Micromesistius poutassou*	340362.7	370044.5	5061.86	6399.77	100.0
Y	Y	Mkit	*Microstomus kitt*	700.4	3098.6	5.26	20.65	20.7
Y	Y	Mdip	*Molva dipterygia*	1275.1	3076.8	2.92	4.47	68.6
Y	Y	Mmol	*Molva molva*	1564.1	3259.0	0.66	1.28	32.0
Y	Y	Mmor	*Mora moro*	855.4	3337.4	2.92	8.46	23.1
Y	Y	Nnor	*Nephrops norvegicus*	755.6	1760.6	21.98	58.58	46.7
Y	Y	Pble	*Phycis blennoides*	10442.2	12233.3	30.93	29.71	90.5
Y	Y	Pvir	*Pollachius virens*	648.5	3064.2	0.28	1.12	12.4
Y	Y	Ssco	*Scomber scombrus*	40.5	303.5	0.64	7.47	4.1
Y	Y	Scan	*Scyliorhinus canicula*	472.1	1142.7	0.44	1.08	21.3
Y	Y	Srin	*Scymnodom ringens*	903.4	4592.9	0.32	1.85	6.5
Y	Y	Tsag	*Todarodes sagittatus*	693.4	1406.3	1.86	3.37	47.9
Y	Y	Tebl	*Todaropsis eblanae*	111.2	290.0	0.69	1.88	26.0
Y	Y	Ttra	*Trachurus trachurus*	25355.7	99206.9	142.48	725.07	57.4
Y	Y	Tesm	*Trisopterus esmarkii*	548.4	2879.3	13.03	67.99	34.3
Y	Y	Tmin	*Trisopterus minutus*	122.2	798.7	2.15	14.35	4.7
N	Y	Aric	*Actinauge richardi*	2529.1	8886.3	229.23	1036.30	75.1

				Biomass (gr)		Number		% Pres
C	**Tot**	**Code**	**Scientific name**	**Avg.**	**Std. Dev.**	**Avg.**	**Std. Dev.**	
N	Y	Aros	*Alepocephalus rostratus*	119.6	883.5	0.22	1.73	2.4
N	Y	Acar	*Aphanopus carbo*	322.7	3397.0	0.40	3.72	6.5
N	Y	Aacu	*Aphrodita aculeata*	42.4	86.7	0.90	1.93	29.0
N	Y	Aolf	*Argyropelecus olfersii*	0.9	3.0	0.30	0.84	16.6
N	Y	Aimp	*Arnoglossus imperialis*	45.9	280.3	3.49	21.54	6.5
N	Y	Airr	*Astropecten irregularis*	82.4	468.2	5.64	22.02	52.1
N	Y	Bmar	*Bathynectes maravigna*	4.3	17.0	0.18	0.54	11.8
N	Y	Cmac	*Callionymus maculatus*	35.5	218.0	2.83	18.34	16.6
N	Y	Cape	*Capros aper*	1496.8	9165.7	28.29	178.54	43.8
N	Y	Cnig	*Centrolophus niger*	93.8	548.6	0.09	0.49	4.7
N	Y	Ccuc	*Chelidonichthys cuculus*	153.4	1111.1	0.95	6.79	3.6
N	Y	Cmon	*Chimaera monstrosa*	10772.7	62788.7	9.93	53.12	40.8
N	Y	Ccid	*Cidaris cidaris*	1930.6	9049.7	62.45	328.96	13.6
N	Y	Ccoe	*Coelorhynchus coelorhynchus*	6699.7	15194.0	100.46	208.51	75.7
N	Y	Crup	*Coryphaenoides rupestris*	772.9	4269.4	0.86	4.92	6.5
N	Y	Dbon	*Dichelopandalus bonnieri*	317.6	796.4	64.79	155.23	74.6
N	Y	Eacu	*Echinus acutus*	493.9	2859.0	23.63	124.01	47.3
N	Y	Ecir	*Eledone cirrhosa*	306.5	703.2	3.27	7.99	49.1
N	Y	Eaeq	*Entelerus aequoraeus*	5.4	9.6	3.19	6.93	50.9
N	Y	Etel	*Epigonus telescopus*	880.3	4567.1	5.62	26.16	21.9
N	Y	Garg	*Gadiculus argenteus*	9956.7	19527.4	443.11	832.61	76.3
N	Y	Gmac	*Gaidropsarus macrophthalmus*	13.9	42.1	0.47	1.28	23.1
N	Y	Glon	*Geryon longipes*	5266.0	13825.0	37.62	99.92	30.8
N	Y	Grho	*Goneplax rhomboides*	1.8	5.0	0.94	2.94	24.3
N	Y	Hjoh	*Halargyreus johnsonii*	12.0	61.4	1.43	7.00	10.1
N	Y	Hsan	*Herincia sanguinolenta*	13.7	69.0	0.31	1.17	16.0
N	Y	Hita	*Hymenocephalus italicus*	2.7	17.4	0.24	1.53	5.9
N	Y	Lsp.	*Lampadena* sp.	3.3	12.8	0.28	1.03	11.8
N	Y	Lcro	*Lampanyctus crocodilus*	11.5	36.8	1.01	3.12	21.9
N	Y	Lcir	*Leucoraja circularis*	263.2	1138.5	0.11	0.51	6.5
N	Y	Lsar	*Luidia sarsi*	1797.9	4324.3	26.66	59.83	58.6
N	Y	Mtub	*Macropipus tuberculatus*	63.5	173.5	3.81	10.84	37.3
N	Y	Mten	*Macropodia tenuirrostris*	5.4	26.7	1.18	2.23	39.1
N	Y	Mlae	*Malacocephalus laevis*	1702.4	2583.3	11.76	21.78	66.9
N	Y	Msar	*Munida sarsi*	2070.2	8355.8	121.36	425.39	39.6
N	Y	Mpun	*Myctophum punctatum*	6.6	30.2	2.72	14.84	23.7
N	Y	Naeq	*Nezumia aequalis*	358.7	2173.9	5.85	32.43	8.3
N	Y	Nscl	*Nezumia sclerorhynchus*	372.4	1818.5	6.08	26.99	8.9
N	Y	Nbon	*Notacanthus bonapartei*	62.8	300.9	0.59	2.61	13.6
N	Y	Ooph	*Ophiura ophiura*	16.9	50.8	2.05	6.29	27.8
N	Y	Pala	*Pagurus alatus*	198.6	337.2	12.61	24.03	84.0
N	Y	Ppri	*Pagurus prideaux*	15.0	65.7	1.45	6.34	13.0
N	Y	Pcor	*Paralepis coregonoides*	1.1	3.9	0.22	0.78	10.7
N	Y	Pmem	*Paraliparis membranaceus*	0.7	4.5	0.19	1.02	5.9
N	Y	Pcuv	*Paromola cuvieri*	397.5	933.0	0.56	1.38	26.6
N	Y	Pmul	*Pasiphaea multidentata*	24.8	117.1	7.20	38.96	10.1
N	Y	Psiv	*Pasiphaea sivado*	32.9	131.7	28.54	177.12	18.3
N	Y	Ppla	*Phormosoma placenta*	3842.3	11940.8	52.28	169.85	23.7
N	Y	Ptyp	*Polycheles typhlops*	2.7	9.7	0.60	2.44	15.4
N	Y	Pnor	*Pontophilus norvegicus*	3.3	10.2	4.14	13.39	33.7
N	Y	Pspi	*Pontophilus spinosus*	1.5	5.1	1.46	6.05	17.2
N	Y	Pcan	*Processa canaliculata*	0.7	2.0	0.44	1.36	16.0
N	Y	Rcar	*Rochinia carpenteri*	6.5	32.2	0.63	2.97	18.9
N	Y	Rmac	*Rossia macrosoma*	21.6	53.3	1.58	4.34	32.5
N	Y	Slig	*Scaphander lignarius*	4.0	8.8	1.36	3.23	33.1
N	Y	Smem	*Solenocera membranacea*	1.9	6.8	0.83	2.82	24.3
N	Y	Spur	*Spatangus purpureus*	5381.3	25555.3	50.51	255.04	37.3
N	Y	Saca	*Squalus acanthias*	304.5	1608.6	0.12	0.68	5.3
N	Y	Stre	*Stichopus tremulus*	13383.7	57858.7	69.38	311.64	76.9
N	Y	Sboa	*Stomias boa*	2.3	9.4	0.29	0.79	16.0
N	Y	Skau	*Synaphobranchus kaupi*	24.1	83.8	3.78	9.93	24.9
N	Y	Tsca	*Trachyrhynchus scabrus*	2180.8	15598.8	7.08	47.24	18.3
N	Y	Xcop	*Xenodermichthys copei*	3.8	17.7	0.60	3.21	10.7
N	N	-	*Acantephyra purpurea*	0.1	0.6	0.07	0.38	4.1
N	N	-	*Ampharetidae undeterminated*	0.0	0.2	0.01	0.08	0.6
N	N	-	*Amphiura chiajei*	0.0	0.3	0.01	0.08	0.6
N	N	-	*Anapagurus laevis*	0.0	0.3	0.04	0.22	3.0
N	N	-	*Ancistrocheirus lesueunii*	0.1	1.2	0.01	0.08	0.6
N	N	-	*Aporrhais pespelicani*	0.2	1.9	0.09	0.79	3.0
N	N	-	*Aporrhais serresianus*	4.2	50.9	0.62	6.49	5.3

				Biomass (gr)		Number		% Pres
C	**Tot**	**Code**	**Scientific name**	**Avg.**	**Std. Dev.**	**Avg.**	**Std. Dev.**	
N	N	-	*Argyropelecus hemigymnus*	0.1	0.4	0.07	0.46	3.6
N	N	-	*Aristeus antenatus*	0.2	1.7	0.02	0.13	1.8
N	N	-	*Arminia trigina*	0.0	0.1	0.01	0.08	0.6
N	N	-	*Asterias rubens*	7.8	50.4	0.17	0.92	6.5
N	N	-	*Asteronyx loveni*	2.2	7.9	0.16	0.52	10.7
N	N	-	*Atelecyclus rotundatus*	0.3	1.4	0.05	0.21	4.7
N	N	-	*Bathypolipus arcticus*	27.1	111.2	0.23	0.88	8.9
N	N	-	*Bathypolipus sponsalis*	30.5	106.6	0.17	0.58	11.8
N	N	-	*Beryx decadactylus*	8.9	69.5	0.02	0.19	1.8
N	N	-	*Beryx splendens*	12.5	79.3	0.04	0.28	3.0
N	N	-	*Brisinga endecacnemos?*	657.5	5986.7	59.17	629.98	5.9
N	N	-	*Brissopsis lyrifera*	0.1	1.3	0.05	0.62	1.2
N	N	-	*Brosme brosme*	45.5	454.5	0.01	0.11	1.2
N	N	-	*Buccinum humphreysianum*	1.3	5.7	0.10	0.42	7.7
N	N	-	*Calliactis parasitica*	1.3	10.9	0.31	2.95	2.4
N	N	-	*Callionymus lyra*	1.6	10.7	0.02	0.15	2.4
N	N	-	*Calliostoma granulatum*	6.0	46.0	0.07	0.48	2.4
N	N	-	*Calocaris macandrae*	0.2	1.1	0.15	0.60	8.3
N	N	-	*Cancer bellianus*	8.7	97.0	0.02	0.13	1.8
N	N	-	*Cancer pagurus*	10.5	96.3	0.01	0.11	1.2
N	N	-	*Centrophorus squamosus*	146.3	1359.0	0.02	0.17	1.2
N	N	-	*Cerianthus lloydii*	0.1	1.0	0.01	0.11	1.2
N	N	-	*Charonia lampax*	3.1	23.7	0.03	0.25	1.8
N	N	-	*Chauliodus sloani*	1.8	10.1	0.12	0.80	4.1
N	N	-	*Chaunax pictus*	14.7	124.5	0.02	0.13	1.8
N	N	-	*Chiasmodon* spp.	0.3	3.4	0.01	0.08	0.6
N	N	-	*Chlorophthalmus agassizii*	0.2	2.8	0.01	0.08	0.6
N	N	-	*Cirolana cranchii*	0.0	0.3	0.01	0.08	0.6
N	N	-	*Citharus linguatula*	0.1	1.2	0.01	0.08	0.6
N	N	-	*Colus* spp.	6.2	26.0	0.21	0.80	11.8
N	N	-	*Corella paralelograma*	0.1	0.8	0.01	0.08	0.6
N	N	-	*Cyttopsis roseus*	0.4	3.3	0.01	0.11	1.2
N	N	-	*Delectopecten vitreus*	0.0	0.2	0.02	0.24	1.2
N	N	-	*Dendrophyllia ramea*	316.3	4106.4	137.34	1785.38	1.2
N	N	-	*Diazona violacea*	0.1	0.5	0.01	0.11	1.2
N	N	-	*Dipturus nidarosiensis*	203.2	2641.5	0.01	0.08	0.6
N	N	-	*Echinus esculentus*	0.2	2.3	0.02	0.23	0.6
N	N	-	*Echinus melo*	73.9	821.0	0.18	1.19	3.6
N	N	-	*Echiodon dentatus*	2.7	12.1	0.46	2.03	9.5
N	N	-	*Epizoanthus incrustatus*	0.1	0.9	0.06	0.36	3.6
N	N	-	*Epizoanthus paguriphilus*	44.0	269.6	1.07	6.45	5.9
N	N	-	*Eunicella verrucosa*	0.6	5.2	0.03	0.17	3.0
N	N	-	*Funchalia woodwardi*	0.2	2.0	0.01	0.08	0.6
N	N	-	*Funiculina quadrangularis*	9.7	78.1	0.69	3.23	11.2
N	N	-	*Galathea strigosa*	0.0	0.2	0.04	0.20	4.1
N	N	-	*Galeodea rugosa*	23.8	77.9	0.34	1.19	14.8
N	N	-	*Galeus murinus*	5.8	75.5	0.02	0.23	0.6
N	N	-	*Geryon affinis*	8.9	115.4	0.02	0.23	0.6
N	N	-	*Griphus vitreus*	0.0	0.2	0.01	0.15	0.6
N	N	-	*Haliphron atlanticus*	291.0	2204.6	0.07	0.28	6.5
N	N	-	*Histioteuthis bonnellii*	7.9	102.3	0.01	0.08	0.6
N	N	-	*Histioteuthis reversa*	4.7	20.1	0.09	0.37	7.1
N	N	-	*Hydrolagus mirabilis*	169.6	2169.0	0.27	3.39	1.2
N	N	-	*Inachus leptochirus*	0.8	3.5	0.13	0.60	7.1
N	N	-	*Laetmonice filicornis*	0.0	0.4	0.01	0.08	0.6
N	N	-	*Lepidopus caudatus*	0.5	4.7	0.01	0.11	1.2
N	N	-	*Leptometra celtica*	0.3	1.9	0.14	0.91	4.1
N	N	-	*Leucoraja fulhonica*	7.0	91.5	0.01	0.15	0.6
N	N	-	*Limanda limanda*	0.3	4.0	0.01	0.08	0.6
N	N	-	*Liocarcinus marmoreus*	0.4	3.3	0.12	1.24	2.4
N	N	-	*Loligo vulgaris*	19.7	116.1	0.05	0.24	4.1
N	N	-	*Luidia ciliaris*	111.3	755.3	1.18	6.55	8.3
N	N	-	*Lunatia fusca*	0.1	0.6	0.02	0.13	1.8
N	N	-	*Lytocarpia myriophyllum*	0.0	0.2	0.01	0.11	1.2
N	N	-	*Macropodia longipes*	0.1	0.8	0.03	0.28	1.2
N	N	-	*Macroramphosus scolopax*	0.4	4.6	0.01	0.15	0.6
N	N	-	*Maurolicus muelleri*	0.1	0.3	0.04	0.19	3.6
N	N	-	*Melanostomias bartonbeani*	0.2	2.2	0.01	0.11	1.2
N	N	-	*Monodaeus couchii*	0.5	2.5	0.24	1.22	11.2
N	N	-	*Munida intermedia*	1.2	13.1	0.05	0.54	1.2

				Biomass (gr)		Number		% Pres
C	**Tot**	**Code**	**Scientific name**	**Avg.**	**Std. Dev.**	**Avg.**	**Std. Dev.**	
N	N	-	*Mustelus asterias*	10.7	139.5	0.01	0.08	0.6
N	N	-	*Nemichthys scolopaceus*	2.3	13.2	0.09	0.53	4.7
N	N	-	*Neorossia caroli*	0.4	4.6	0.04	0.54	0.6
N	N	-	*Neptunea contraria*	31.4	165.7	0.79	3.99	13.0
N	N	-	*Neptunea despecta*	96.0	545.0	0.44	2.04	11.2
N	N	-	*Notoscopelus kroeyerii*	1.6	12.9	0.21	2.12	3.0
N	N	-	*Nymphaster arenatus*	44.7	209.5	1.09	5.31	13.6
N	N	-	*Octopus defilippi*	3.4	25.7	0.02	0.13	1.8
N	N	-	*Odontaster mediterraneus*	2.6	23.0	0.12	1.04	3.6
N	N	-	*Ophiothrix fragilis*	182.6	1790.9	33.82	350.94	5.3
N	N	-	*Opistoteuthis agassizii*	9.5	123.7	0.01	0.15	0.6
N	N	-	*Pagurus bernhardus*	3.0	19.3	0.04	0.23	3.6
N	N	-	*Pagurus carneus*	0.6	4.9	0.03	0.23	1.8
N	N	-	*Parapagurus pilosimanus*	60.6	343.6	2.69	12.53	8.3
N	N	-	*Pennatula rubra*	0.4	2.2	0.33	1.69	6.5
N	N	-	*Phakelia ventilabrum*	2.7	21.3	0.05	0.42	1.8
N	N	-	*Plesionika heterocarpus*	5.0	65.2	1.05	13.69	0.6
N	N	-	*Polybius henslowi*	0.2	1.6	0.01	0.11	1.2
N	N	-	*Polymetne corythaeola*	0.8	4.8	0.04	0.19	3.6
N	N	-	*Polynoidae undeterminated*	0.0	0.2	0.03	0.20	2.4
N	N	-	*Pontaster tenuispinus*	1.1	6.2	0.12	0.62	4.7
N	N	-	*Porania pulvillus*	72.2	897.9	0.77	8.70	7.1
N	N	-	*Porania stormi*	2.3	19.8	0.02	0.19	1.8
N	N	-	*Pseudamussium septenradiatum*	0.0	0.2	0.01	0.08	0.6
N	N	-	*Pseudarchaster gracilis*	1.6	20.6	0.03	0.38	0.6
N	N	-	*Psilaster andromeda*	40.0	251.7	2.16	14.43	6.5
N	N	-	*Pycnogonum littorale*	0.3	1.0	0.36	1.49	12.4
N	N	-	*Raja clavata*	38.2	496.9	0.01	0.08	0.6
N	N	-	*Raja montagui*	9.8	127.1	0.01	0.08	0.6
N	N	-	*Rajella fyllae*	29.4	341.6	0.07	0.77	1.2
N	N	-	*Rhinonemus cimbrius*	2.5	19.3	0.04	0.26	2.4
N	N	-	*Rondeletiola minor*	0.5	2.1	0.35	1.54	12.4
N	N	-	*Scalpellum scalpellum*	0.2	0.8	0.08	0.41	4.7
N	N	-	*Scotoplanes* sp.*?*	133.8	1072.2	1.77	16.11	8.9
N	N	-	*Sebastes viviparus*	1.1	14.0	0.01	0.08	0.6
N	N	-	*Sepia elegans*	0.1	0.8	0.01	0.08	0.6
N	N	-	*Sepia officinalis*	0.0	0.3	0.01	0.08	0.6
N	N	-	*Sepietta* sp.	3.6	11.5	0.88	2.49	21.9
N	N	-	*Sergestes arcticus*	1.1	7.1	0.57	3.55	5.3
N	N	-	*Serrivomer beanii*	0.0	0.2	0.01	0.08	0.6
N	N	-	*Sipunculida*	0.0	0.4	0.01	0.08	0.6
N	N	-	*Solea vulgaris*	4.6	59.8	0.01	0.15	0.6
N	N	-	*Spirontocaris spinus*	0.0	0.4	0.01	0.08	0.6
N	N	-	*Suberites* sp.	4.0	18.2	0.32	1.38	9.5
N	N	-	*Trachipterus arcticus*	5.7	73.5	0.01	0.08	0.6
N	N	-	*Trachyscorpia cristulata echinata*	12.9	166.5	0.02	0.17	1.2
N	N	-	*Troschelia berniciensis*	54.1	145.3	0.96	2.65	25.4
N	N	-	*Zeus faber*	11.4	148.3	0.01	0.08	0.6

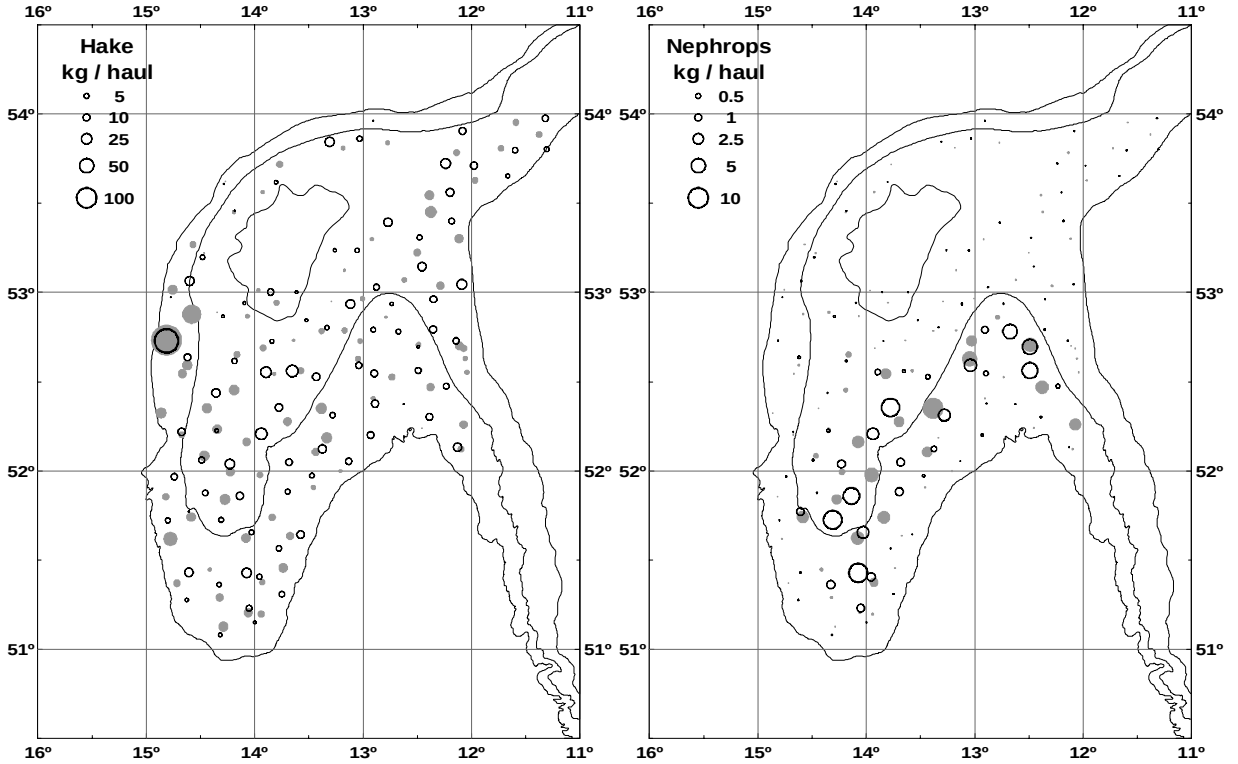

Figure 1. Hake and nephrops catch distribution in biomass (kg/30 min haul) during survey Porcupine 2001 (grey circles) and 2002 (empty circles)

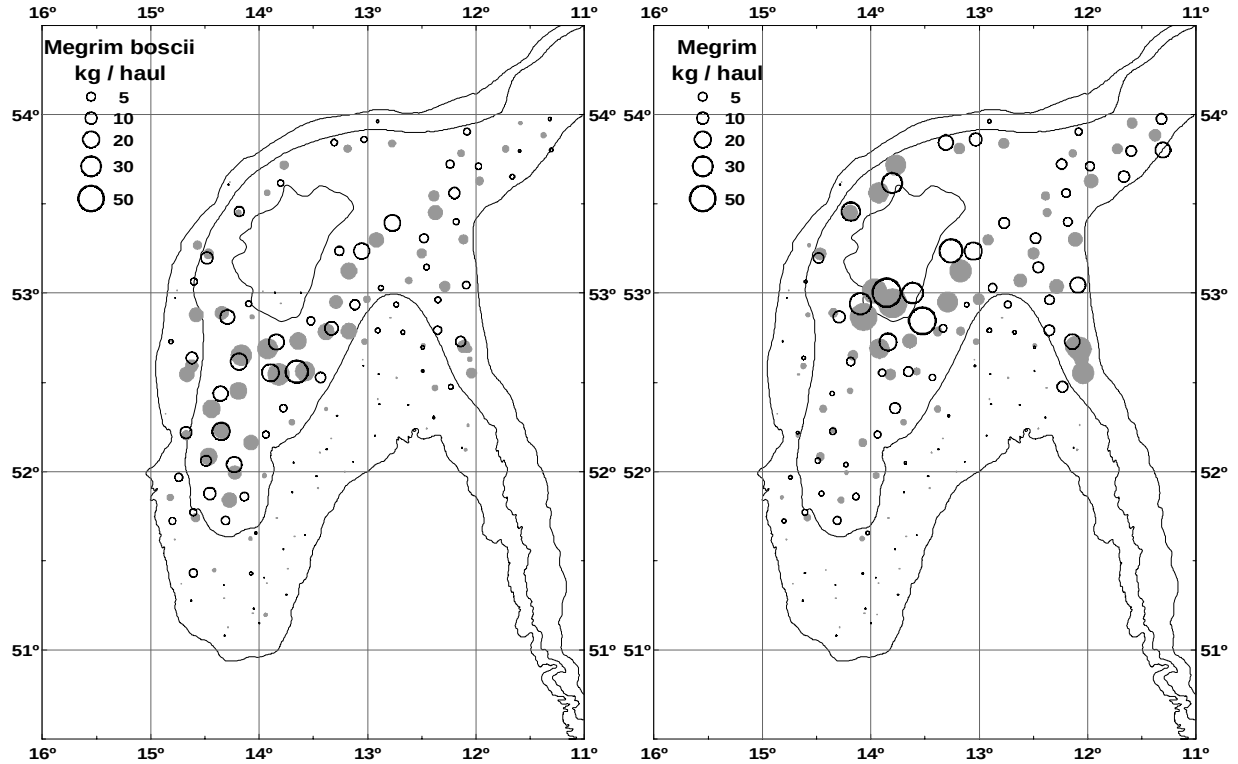

Figure 2. Four spotted megrim (*L. boscii*) and megrim catch distribution in biomass (kg/30 min haul) during survey Porcupine 2001 (grey circles) and 2002 (empty circles)

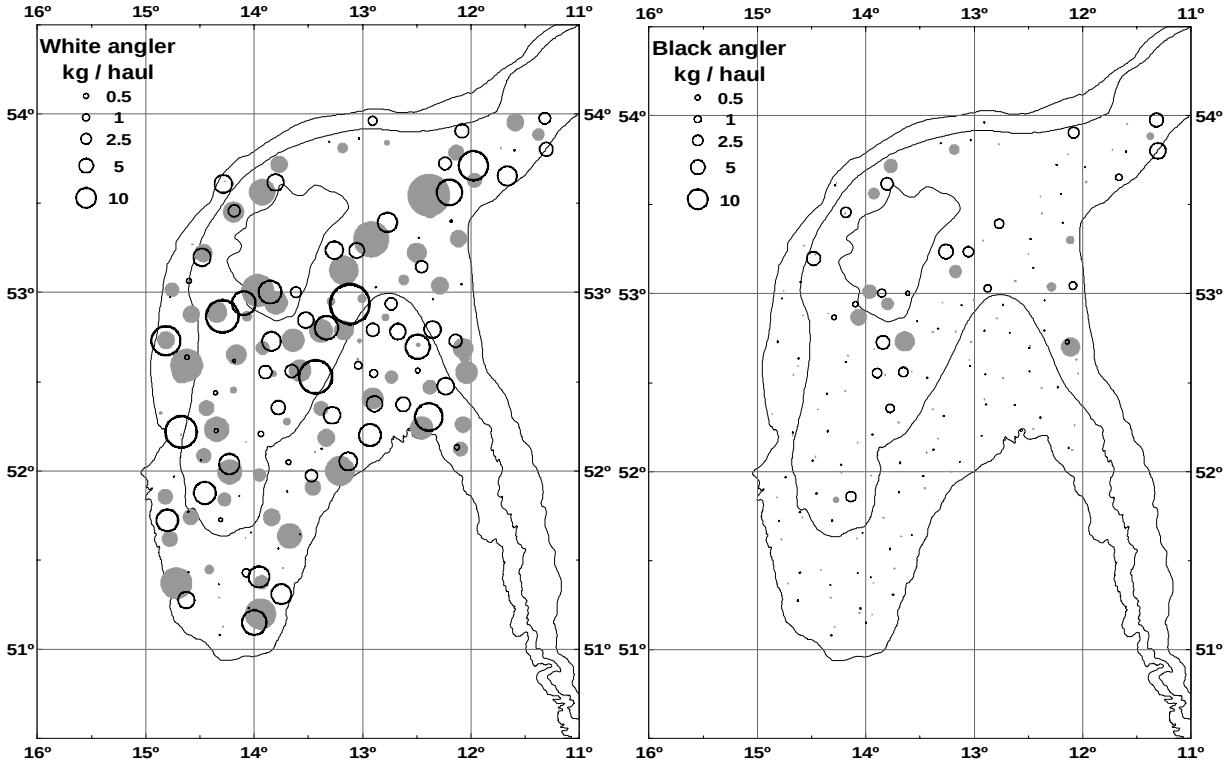

Figure 3. Anglers (*L. budegassa* and *L. piscatorius*) catch distribution in biomass (kg/30 min haul) during survey Porcupine 2001 (grey circles) and 2002 (empty circles)

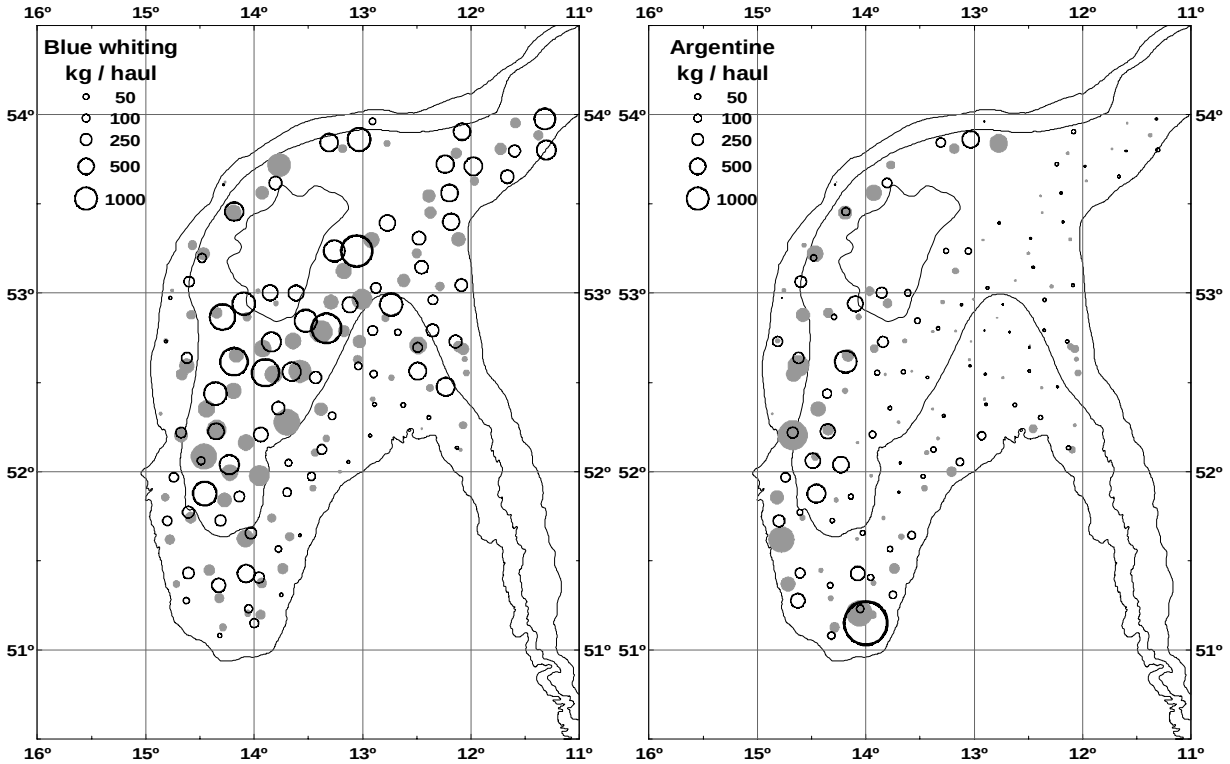

Figure 4. Blue whiting and argentine catch distribution in biomass (kg/30 min haul) during survey Porcupine 2001 (grey circles) and 2002 (empty circles)

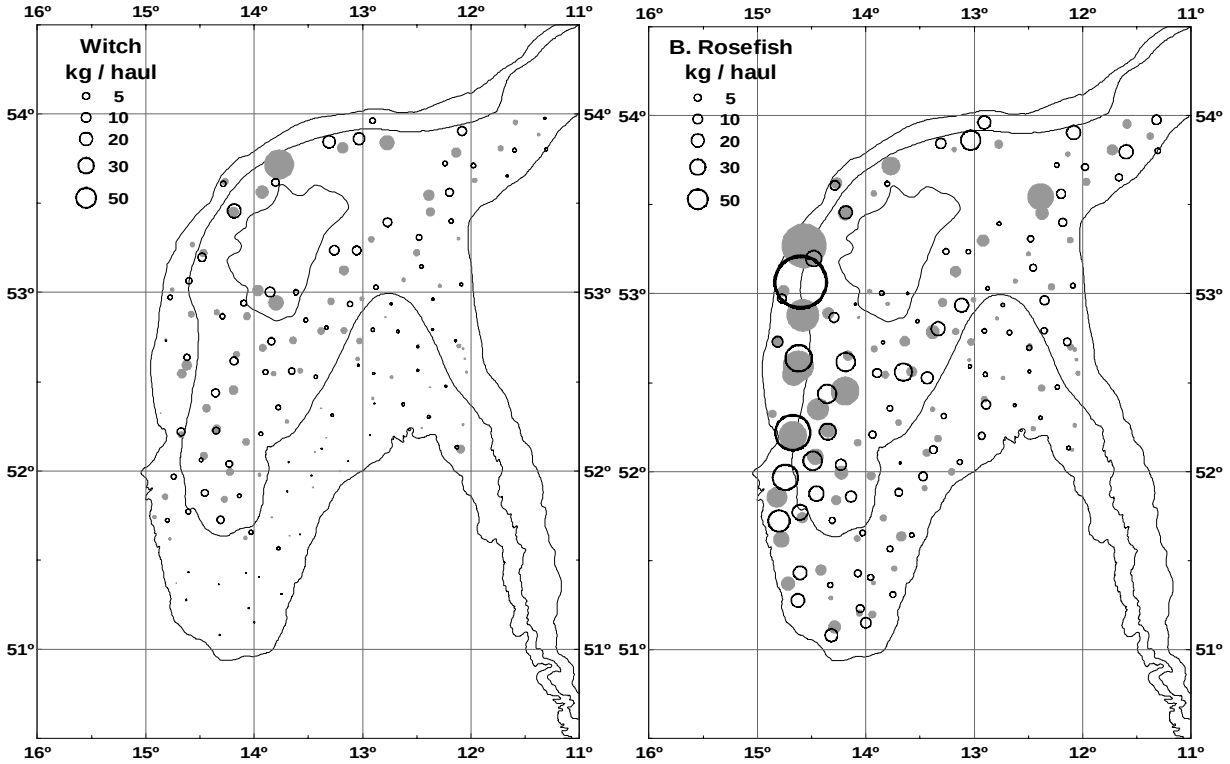

Figure 5. Witch and blackbelly rosefish catch distribution in biomass (kg/30 min haul) during survey Porcupine 2001 (grey circles) and 2002 (empty circles)

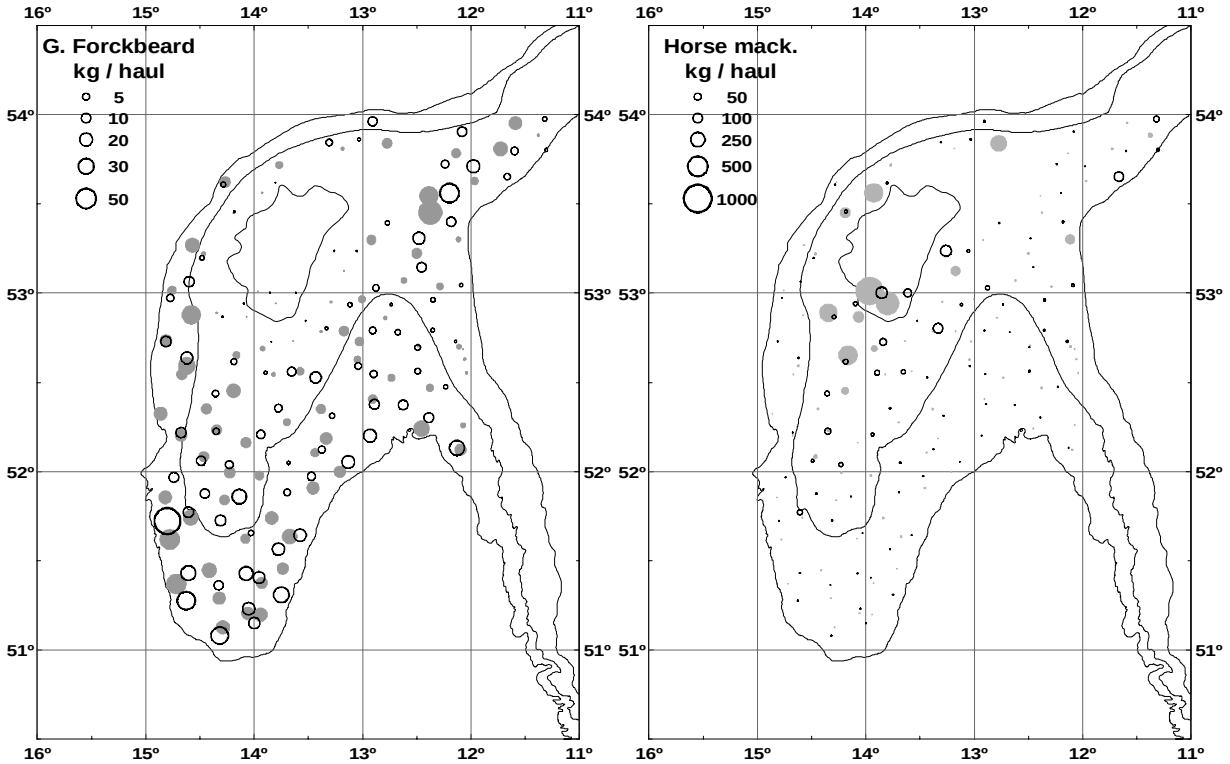

Figure 6. Greater forkbeard and horse mackerel catch distribution in biomass (kg/30 min haul) during survey Porcupine 2001 (grey circles) and 2002 (empty circles)

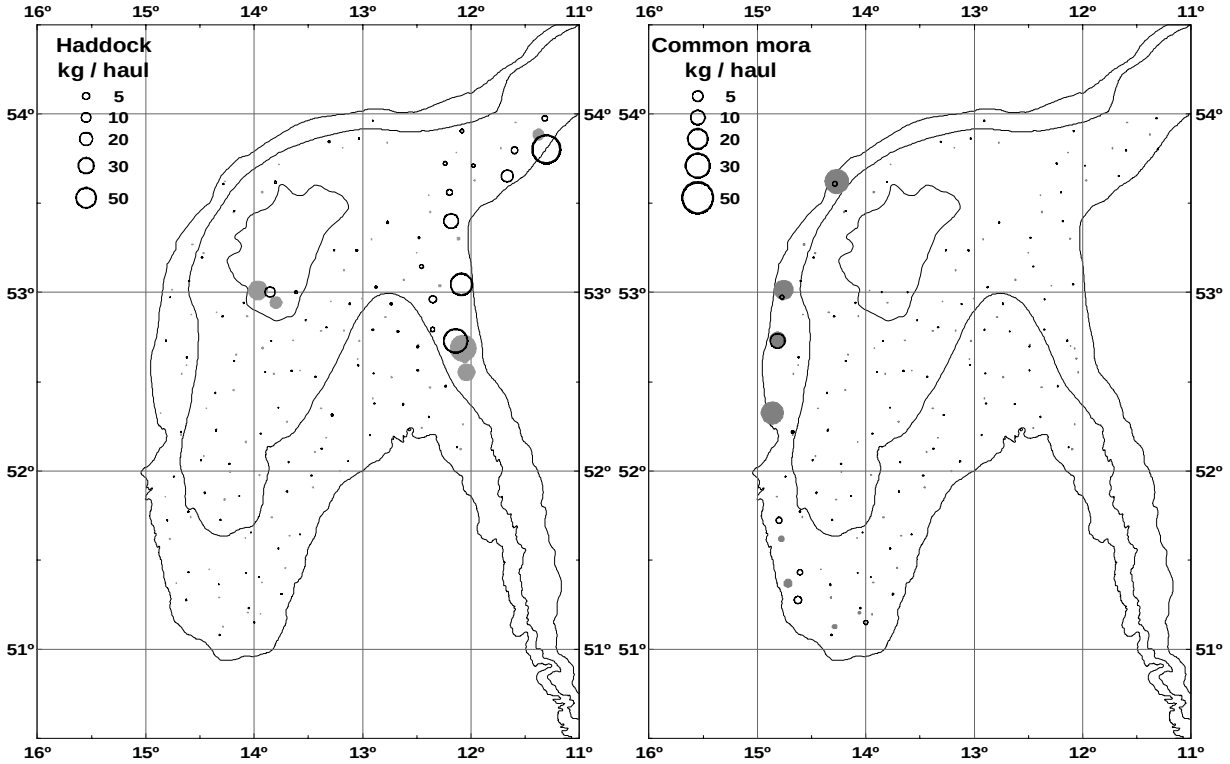

Figure 7. Haddock and common mora catch distribution in biomass (kg/30 min haul) during survey Porcupine 2001 (grey circles) and 2002 (empty circles)